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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/779,050B

DATE: 02/24/2003 P6
TIME: 13:48:48

Input Set : A:\A-570B.txt
Output Set: N:\CRF4\02242003\I779050B.raw

3 <110> APPLICANT: BOYLE, WILLIAM J.
4 HSU, HAILING
6 <120> TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
8 <130> FILE REFERENCE: A-570B
10 <140> CURRENT APPLICATION NUMBER: 09/779,050B
C--> 11 <141> CURRENT FILING DATE: 2000-02-12
13 <150> PRIOR APPLICATION NUMBER: 60/181,800
14 <151> PRIOR FILING DATE: 2000-02-11
16 <160> NUMBER OF SEQ ID NOS: 52
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1173
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (143)..(997)
28 <223> OTHER INFORMATION:
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33 acaaacacag ataacaggaa atgatccatt ccctgtggc acttattcta aaggccccaa 120
35 cttcaaaat tcaagtagtg at atg gat gac tcc aca gaa agg gag cag tca 172
36 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser
37 1 5 10
39 cgc ctt act tct tgc ctt aag aaa aga gaa atg aaa ctg aag gag 220
40 Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys Glu
41 15 20 25
43 tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc tcc 268
44 Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser Ser
45 30 35 40
47 aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg tct 316
48 Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Ala Leu Leu Ser
49 45 50 55
51 tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa ggg 364
52 Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly
53 60 65 70
55 gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag aag 412
56 Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu Lys
57 75 80 85 90
59 ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct cca 460
60 Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro
61 95 100 105
63 gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga gaa 508

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64	Ala	Val	Thr	Ala	Gly	Leu	Lys	Ile	Phe	Glu	Pro	Pro	Ala	Pro	Gly	Glu	
65				110			115							120			
67	ggc	aac	tcc	agt	cag	aac	agc	aga	aat	aag	cgt	gcc	gtt	cag	ggt	cca	556
68	Gly	Asn	Ser	Ser	Gln	Asn	Ser	Arg	Asn	Lys	Arg	Ala	Val	Gln	Gly	Pro	
69				125			130							135			
71	gaa	gaa	aca	gtc	act	caa	gac	tgc	ttg	caa	ctg	att	gca	gac	agt	gaa	604
72	Glu	Glu	Thr	Val	Thr	Gln	Asp	Cys	Leu	Gln	Leu	Ile	Ala	Asp	Ser	Glu	
73				140			145							150			
75	aca	cca	act	ata	caa	aaa	gga	tct	tac	aca	ttt	gtt	cca	tgg	ctt	ctc	652
76	Thr	Pro	Thr	Ile	Gln	Lys	Gly	Ser	Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu	
77	155				160					165				170			
79	agc	ttt	aaa	agg	gga	agt	gcc	cta	gaa	gaa	aaa	gag	aat	aaa	ata	ttg	700
80	Ser	Phe	Lys	Arg	Gly	Ser	Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Leu	
81				175			180							185			
83	gtc	aaa	gaa	act	ggt	tac	ttt	ttt	ata	tat	ggt	cag	gtt	tta	tat	act	748
84	Val	Lys	Glu	Thr	Gly	Tyr	Phe	Phe	Ile	Tyr	Gly	Gln	Val	Leu	Tyr	Thr	
85				190			195							200			
87	gat	aag	acc	tac	gcc	atg	gga	cat	cta	att	cag	agg	aag	aag	gtc	cat	796
88	Asp	Lys	Thr	Tyr	Ala	Met	Gly	His	Leu	Ile	Gln	Arg	Lys	Lys	Val	His	
89				205			210							215			
91	gtc	ttt	ggg	gat	gaa	ttg	agt	ctg	gtg	act	ttg	ttt	cga	tgt	att	caa	844
92	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	
93	220				225			230									
95	aat	atg	cct	gaa	aca	cta	ccc	aat	aat	tcc	tgc	tat	tca	gct	ggc	att	892
96	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn	Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Ile	
97	235				240			245							250		
99	gca	aaa	ctg	gaa	gaa	gga	gat	gaa	ctc	caa	ctt	gca	ata	cca	aga	gaa	940
100	Ala	Lys	Leu	Glu	Glu	Gly	Asp	Glu	Leu	Gln	Leu	Ala	Ile	Pro	Arg	Glu	
101				255			260							265			
103	aat	gca	caa	ata	tca	ctg	gat	gga	gat	gtc	aca	ttt	ttt	ggt	gca	ttg	988
104	Asn	Ala	Gln	Ile	Ser	Leu	Asp	Gly	Asp	Val	Thr	Phe	Phe	Gly	Ala	Leu	
105				270			275							280			
107	aaa	ctg	ctg	tgacctactt	acaccatgtc	tgttagctatt	ttcctccctt									1037	
108	Lys	Leu	Leu														
109		285															
111	tctctgtacc	tctaagaaga	aagaatctaa	ctgaaaatac	aaaaaaaaaaa	1097											
113	aaaaaaaaaaa	agttaaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	1157	
115	aaaaaactcg	ggg	aggggg													1173	
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119	<211>	LENGTH:	285														
120	<212>	TYPE:	PRT														
121	<213>	ORGANISM:	Homo sapiens														
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126	1				5				10						15		
129	Lys	Lys	Arg	Glu	Glu	Met	Lys	Leu	Lys	Glu	Cys	Val	Ser	Ile	Leu	Pro	
130					20				.25						30		
133	Arg	Lys	Glu	Ser	Pro	Ser	Val	Arg	Ser	Ser	Lys	Asp	Gly	Lys	Leu	Leu	
134					35				40						45		

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137 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 138 50 55 60
 141 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 142 65 70 75 80
 145 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
 146 85 90 95
 149 Ala Pro Lys Ala Gly Leu Glu Ala Pro Ala Val Thr Ala Gly Leu
 150 100 105 110
 153 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
 154 115 120 125
 157 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
 158 130 135 140
 161 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
 162 145 150 155 160
 165 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
 166 165 170 175
 169 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
 170 180 185 190
 173 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
 174 195 200 205
 177 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
 178 210 215 220
 181 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
 182 225 230 235 240
 185 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
 186 245 250 255
 189 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
 190 260 265 270
 193 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 194 275 280 285

197 <210> SEQ ID NO: 3
 198 <211> LENGTH: 1139
 199 <212> TYPE: DNA
 200 <213> ORGANISM: Mus musculus
 202 <220> FEATURE:
 203 <221> NAME/KEY: CDS
 204 <222> LOCATION: (52)..(978)
 205 <223> OTHER INFORMATION:

W--> 207 <400> 3

208 gaattcggca cgagctccaa aggcttagac cttcaaagtg ctccctcggtgg a atg gat 57
 209 Met Asp
 210 1
 212 gag tct gca aag acc ctg cca cca ccg tgc ctc tgt ttt tgc tcc gag 105
 213 Glu Ser Ala Lys Thr Leu Pro Pro Cys Leu Cys Phe Cys Ser Glu
 214 5 10 15
 216 aaa gga gaa gat atg aaa gtg gga tat gat ccc atc act ccg cag aag 153
 217 Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro Gln Lys
 218 20 25 30
 220 gag gag ggt gcc tgg ttt ggg atc tgc agg gat gga agg ctg ctg gct 201

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221	Glu	Glu	Gly	Ala	Trp	Phe	Gly	Ile	Cys	Arg	Asp	Gly	Arg	Leu	Leu	Ala	
222	35				40				45						50		
224	gct	acc	ctc	ctg	ctg	gcc	ctg	ttg	tcc	agc	agt	ttc	aca	gct	atg	tcc	249
225	Ala	Thr	Leu	Leu	Leu	Ala	Leu	Leu	Ser	Ser	Ser	Ser	Phe	Thr	Ala	Met	Ser
226					55				60						65		
228	ttg	tac	cag	ttg	gct	gcc	ttg	caa	gca	gac	ctg	atg	aac	ctg	cgc	atg	297
229	Leu	Tyr	Gln	Leu	Ala	Ala	Leu	Gln	Ala	Asp	Leu	Met	Asn	Leu	Arg	Met	
230					70				75						80		
232	gag	ctg	cag	agc	tac	cga	ggt	tca	gca	aca	cca	gcc	gcc	gct	ggt	gct	345
233	Glu	Leu	Gln	Ser	Tyr	Arg	Gly	Ser	Ala	Thr	Pro	Ala	Ala	Ala	Gly	Ala	
234					85				90						95		
236	cca	gag	ttg	acc	gct	gga	gtc	aaa	ctc	ctg	aca	ccg	gca	gct	cct	cga	393
237	Pro	Glu	Leu	Thr	Ala	Gly	Val	Lys	Leu	Leu	Thr	Pro	Ala	Ala	Pro	Arg	
238					100				105						110		
240	ccc	cac	aac	tcc	agc	cgc	ggc	cac	agg	aac	aga	cgc	gct	ttc	cag	gga	441
241	Pro	His	Asn	Ser	Ser	Arg	Gly	His	Arg	Asn	Arg	Arg	Arg	Ala	Phe	Gln	Gly
242					115				120						125		130
244	cca	gag	gaa	aca	gaa	caa	gat	gta	gac	ctc	tca	gct	cct	cct	gca	cca	489
245	Pro	Glu	Glu	Thr	Glu	Gln	Asp	Val	Asp	Leu	Ser	Ala	Pro	Pro	Ala	Pro	
246					135				140						145		
248	tgc	ctg	cct	gga	tgc	cgc	cat	tct	caa	cat	gat	gat	aat	gga	atg	aac	537
249	Cys	Leu	Pro	Gly	Cys	Arg	His	Ser	Gln	His	Asp	Asp	Asn	Gly	Met	Asn	
250					150				155						160		
252	ctc	aga	aac	atc	att	caa	gac	tgt	ctg	cag	ctg	att	gca	gac	agc	gac	585
253	Leu	Arg	Asn	Ile	Ile	Gln	Asp	Cys	Leu	Gln	Leu	Ile	Ala	Asp	Ser	Asp	
254					165				170						175		
256	acg	ccg	act	ata	cga	aaa	gga	act	tac	aca	ttt	gtt	cca	tgg	ctt	ctc	633
257	Thr	Pro	Thr	Ile	Arg	Lys	Gly	Thr	Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu	
258					180				185						190		
260	agc	ttt	aaa	aga	aat	gcc	ttg	gag	gag	aaa	gag	aac	aaa	ata	gtg		681
261	Ser	Phe	Lys	Arg	Gly	Asn	Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Val	
262					195				200						205		210
264	gtg	agg	caa	aca	ggc	tat	ttc	ttc	atc	tac	agc	cag	gtt	cta	tac	acg	729
265	Val	Arg	Gln	Thr	Gly	Tyr	Phe	Phe	Ile	Tyr	Ser	Gln	Val	Leu	Tyr	Thr	
266					215				220						225		
268	gac	ccc	atc	ttt	gct	atg	ggt	cat	gtc	atc	cag	agg	aag	aaa	gta	cac	777
269	Asp	Pro	Ile	Phe	Ala	Met	Gly	His	Val	Ile	Gln	Arg	Lys	Lys	Val	His	
270					230				235						240		
272	gtc	ttt	ggg	gac	gag	ctg	agc	ctg	gtg	acc	ctg	ttc	cga	tgt	att	cag	825
273	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	
274					245				250						255		
276	aat	atg	ccc	aaa	aca	ctg	ccc	aac	aat	tcc	tgc	tac	ttg	gct	ggc	atc	873
277	Asn	Met	Pro	Lys	Thr	Leu	Pro	Asn	Asn	Ser	Cys	Tyr	Leu	Ala	Gly	Ile	
278					260				265						270		
280	gct	agg	ctg	gaa	gaa	gga	gat	gag	att	cag	ctt	gca	att	cct	cgg	gag	921
281	Ala	Arg	Leu	Glu	Glu	Gly	Asp	Glu	Ile	Gln	Leu	Ala	Ile	Pro	Arg	Glu	
282					275				280						285		290
284	aat	gca	cag	att	tca	cgc	aac	gga	gac	gac	acc	ttc	ttt	ggt	gcc	cta	969
285	Asn	Ala	Gln	Ile	Ser	Arg	Asn	Gly	Asp	Asp	Thr	Phe	Phe	Gly	Ala	Leu	

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286	295	300	305	
288	aaa ctg ctg taactcactt	gctggaggtgc	gtgatcccct	tccctcgctct
289	Lys Leu	Leu		1018
292	tctctgtacc	tccgagggag	aaacagacga	ctggaaaaat
294	agcggaaagt	ttctcggtac	ccgttgaatc	tgatccaaac
296	c			caggaaatat
299	<210> SEQ ID NO: 4			aacagacago
300	<211> LENGTH: 309			1138
301	<212> TYPE: PRT			1139
302	<213> ORGANISM: Mus musculus			
304	<400> SEQUENCE: 4			
306	Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys			
307	1	5	10	15
310	Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro			
311	20	25	30	
314	Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu			
315	35	40	45	
318	Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala			
319	50	55	60	
322	Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu			
323	65	70	75	80
326	Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala			
327	85	90	95	
330	Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala			
331	100	105	110	
334	Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe			
335	115	120	125	
338	Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro			
339	130	135	140	
342	Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly			
343	145	150	155	160
346	Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp			
347	165	170	175	
350	Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp			
351	180	185	190	
354	Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys			
355	195	200	205	
358	Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu			
359	210	215	220	
362	Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys			
363	225	230	235	240
366	Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys			
367	245	250	255	
370	Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala			
371	260	265	270	
374	Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro			
375	275	280	285	
378	Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly			
379	290	295	300	

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 3,5,6,7,8,9,10,11,12,14,15,17,18,20,22,25,26,27,28,29,30
Seq#:5; Xaa Pos. 31,32,33,34,35,37,38,39,40,41,42,43,44,47,60,61,62,64,65
Seq#:5; Xaa Pos. 67,70,75,78,79,82,86,87,88,89,90,91,92,95,100,101,105,107
Seq#:5; Xaa Pos. 108,109,111,114,115,116,120,121,122,125,128,135,136,147
Seq#:5; Xaa Pos. 152,155,179,181,182,190,197,198,199,204,231,245,252,265
Seq#:5; Xaa Pos. 266,269
Seq#:6; Xaa Pos. 1,8,10,12,15,18,21,23,25,29,39,41,44,47,49,51,53,55,57,60
Seq#:6; Xaa Pos. 64,66,68,70,72,79,81,84,90,92,94
Seq#:25; Xaa Pos. 11,16,19
Seq#:26; Xaa Pos. 5
Seq#:27; Xaa Pos. 11,16,19,33,43,45,46,54,61,62,63,68,95,109,116,129,130
Seq#:27; Xaa Pos. 133

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 393,394
Seq#:6; Line(s) 479
Seq#:27; Line(s) 1405

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:25,26,27

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
L:207 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:205
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
M:341 Repeated in SeqNo=6
L:1363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:1411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:1620 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:41,Line#:1618